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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/877,987

DATE: 11/01/2001

TIME: 14:39:11

Input Set : A:\Townsen1.app

Output Set: N:\CRF3\11012001\I877987.raw

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3 <110> APPLICANT: Townsend, Robert M.
4   Todderud, Charles G
5   Peach, Robert J.
7 <120> TITLE OF INVENTION: METHODS FOR REGULATING A CELL-MEDIATED IMMUNE RESPONSE
8   BY BLOCKING LYMPHOCYTIC SIGNALS AND BY BLOCKING LFA-1
9   MEDIATED ADHESION
11 <130> FILE REFERENCE: D0009NP/30436.53USU1
13 <140> CURRENT APPLICATION NUMBER: 09/877,987
14 <141> CURRENT FILING DATE: 2001-06-08
16 <150> PRIOR APPLICATION NUMBER: 60/210,671
17 <151> PRIOR FILING DATE: 2000-06-09
19 <160> NUMBER OF SEQ ID NOS: 9
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26 <213> ORGANISM: Homo sapiens
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65 <210> SEQ ID NO: 5
66 <211> LENGTH: 42
67 <212> TYPE: DNA
68 <213> ORGANISM: Artificial Sequence
70 <220> FEATURE:

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71 <223> OTHER INFORMATION: Description of Artificial Sequence:Oncostatin M
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84 <223> OTHER INFORMATION: Description of Artificial Sequence:CTLA4Ig
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89 ggcacgccta gctttgtgtg tgagtatgca tctccaggca aagccactga ggtccgggtg 180
90 acagtgtctc gccaggtctg cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
91 gggaatgagt tgaccttcct agatgattcc atctgcacgg gcacctccag tggaaatcaa 300
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122 20 25 30
124 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
125 35 40 45
127 Tyr Ala Ser Pro Gly Lys Ala Thr Glu Val Arg Val Thr Val Leu Arg
128 50 55 60
130 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
131 65 70 75 80
133 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser

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139 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
140          115          120          125
142 Tyr Leu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
143          130          135          140
145 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
146 145          150          155          160
148 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
149          165          170          175
151 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
152          180          185          190
154 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
155          195          200          205
157 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys
158          210          215          220
160 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
161 225          230          235          240
163 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
164          245          250          255
166 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
167          260          265          270
169 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
170          275          280          285
172 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
173          290          295          300
175 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
176 305          310          315          320
178 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
179          325          330          335
181 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
182          340          345          350
184 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
185          355          360          365
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196 <220> FEATURE:
197 <223> OTHER INFORMATION: Description of Artificial Sequence:L104EA29YIq
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202 ggcacgcta gctttgtgtg tgagtatgca tctccaggca aatatactga ggtccgggtg 180
203 acagtgttc ggcaggctga cagccagggtg actgaagtct gtgcggcaac ctacatgatg 240
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205 gtgaacctca ctatccaagg actgagggcc atggacacgg gactctacat ctgcaagggtg 360
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207 attgateccag aaccgtgccc agattctgat caggagccca aatcttctga caaaactcac 480
208 acatccccac cgccccagc acctgaactc ctggggggat cgtcagtctt cctcttcccc 540
209 ccaaaccaca aggacaccct catgatctcc cggaccctg aggtcacatg cgtgggtggtg 600
210 gacgtgagcc acgaagaccc tgaggtcaag ttcaactggt acgtggacgg cgtggaggtg 660
211 cataatgcc aagacaaagcc gcgggaggag cagtacaaca gcacgtaccg tgtggtcagc 720
212 gtccctaccg tccctgcacca ggactggctg aatggcaagg agtacaagtg caaggtctcc 780
213 aacaaagccc tcccagcccc catcgagaaa accatctcca aagccaaagg gcagccccga 840
214 gaaccacagg tgtacaccct gccccatcc cgggatgagc tgaccaagaa ccaggtcagc 900
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235 20 25 30
237 Ala Val Val Leu Ala Ser Ser Arg Gly Ile Ala Ser Phe Val Cys Glu
238 35 40 45
240 Tyr Ala Ser Pro Gly Lys Tyr Thr Glu Val Arg Val Thr Val Leu Arg
241 50 55 60
243 Gln Ala Asp Ser Gln Val Thr Glu Val Cys Ala Ala Thr Tyr Met Met
244 65 70 75 80
246 Gly Asn Glu Leu Thr Phe Leu Asp Asp Ser Ile Cys Thr Gly Thr Ser
247 85 90 95
249 Ser Gly Asn Gln Val Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp
250 100 105 110
252 Thr Gly Leu Tyr Ile Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr
253 115 120 125
255 Tyr Glu Gly Ile Gly Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu
256 130 135 140
258 Pro Cys Pro Asp Ser Asp Gln Glu Pro Lys Ser Ser Asp Lys Thr His
259 145 150 155 160
261 Thr Ser Pro Pro Ser Pro Ala Pro Glu Leu Leu Gly Gly Ser Ser Val
262 165 170 175
264 Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
265 180 185 190
267 Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
268 195 200 205
270 Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys

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273 Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser
274 225      230      235      240
276 Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys
277      245      250      255
279 Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
280      260      265      270
282 Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
283      275      280      285
285 Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
286      290      295      300
288 Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
289 305      310      315      320
291 Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
292      325      330      335
294 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
295      340      345      350
297 Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
298      355      360      365
300 His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
301      370      375      380

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VERIFICATION SUMMARY

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